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SEQUENCE LISTING

<110> International Flower Developments Pty Ltd
 Brugliera, Filippa (US only)
 Demelis, Linda (US only)
 Koes, Ronald (US only)
 Tanaka, Yoshikazu (US only)

<120> Genetic sequences and uses therefor

<130> 2606090/EJH

<140> Not yet available

<141> 2003-01-24

<150> AU PS0174/02

<151> 2002-01-25

<160> 47

<170> PatentIn version 3.1

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<211> 969

<212> DNA

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 aaaaaaaaaa 969

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Lys Tyr Ile Leu Glu Thr Ser Val Tyr Pro Arg Glu His Glu Leu Leu
 35 40 45

Lys Glu Leu Thr Lys Ala Ser Phe Glu Asn Tyr Lys Ala Ala Ser Phe
 50 55 60

Met Gly Leu Pro Gln Asp Glu Ala Gln Phe Leu Ser Met Phe Leu Lys
 65 70 75 80

Leu Ile Asn Ala Lys Lys Thr Leu Glu Ile Gly Val Phe Thr Gly Tyr
 85 90 95

Ser Leu Leu Val Thr Ala Leu Ala Leu Pro Glu Asp Gly Lys Val Ile
 100 105 110

Ala Ile Asp Pro Asp Arg Glu Ala Tyr Glu Val Gly Leu Pro Tyr Ile
 115 120 125

Gln Lys Ala Gly Val Glu His Lys Ile Glu Phe Ile Gln Ser Glu Ala
 130 135 140

Val Pro Val Leu Glu Lys Leu Leu Ser Asn Glu Lys Glu Ala Gly Thr
 145 150 155 160

Phe Asp Phe Val Phe Ile Asp Ala Asp Lys Glu Asn Tyr Leu Lys Tyr
 165 170 175

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His Glu Ile Val Leu Lys Leu Val Lys Val Gly Gly Val Ile Gly Tyr
 180 185 190

Asp Asn Thr Leu Trp Phe Gly Thr Val Ala Leu Ser Glu Asp Asp Pro
 195 200 205

Met Pro Glu Gly Leu Arg Ala Leu Arg Gly His Val Met Lys Val Asn
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Ser Phe Leu Ala Thr Asp Pro Arg Val Glu Val Ala Gln Leu Ser Ile
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Gly Asp Gly Leu Thr Leu Cys Arg Arg Leu Ser
 245 250

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 <213> oligonucleotide

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Ala His Pro Gly Ile Leu Arg Ser Asp Ala Leu Arg Lys Tyr Ile Leu
 35 40 45

Glu Thr Ser Val Tyr Pro Arg Glu His Glu Leu Leu Lys Glu Leu Thr
 50 55 60

Lys Ala Ser Phe Glu Asn Tyr Lys Ala Ala Ser Phe Met Gly Leu Pro
 65 70 75 80

Gln Asp Glu Ala Gln Phe Leu Ser Met Phe Leu Lys Leu Ile Asn Ala
 85 90 95

Lys Lys Thr Leu Glu Ile Gly Val Phe Thr Gly Tyr Ser Leu Leu Val
 100 105 110

Thr Ala Leu Ala Leu Pro Glu Asp Gly Lys Val Ile Ala Ile Asp Pro
 115 120 125

Asp Arg Glu Ala Tyr Glu Val Gly Leu Pro Tyr Ile Gln Lys Ala Gly
 130 135 140

Val Glu His Lys Ile Glu Phe Ile Gln Ser Glu Ala Val Pro Val Leu
 145 150 155 160

Glu Lys Leu Leu Ser Asn Glu Lys Glu Ala Gly Thr Phe Asp Phe Val

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	165		170		175
Phe Ile Asp	Ala Asp Lys Glu Asn Tyr Leu Lys Tyr His Glu Ile Val				
	180		185		190
Leu Lys Leu Val Lys Val Gly Gly Val Ile Gly Tyr Asp Asn Thr Leu					
	195		200		205
Trp Phe Gly Thr Val Ala Leu Ser Glu Asp Asp Pro Met Pro Glu Gly					
	210		215		220
Leu Arg Ala Leu Arg Gly His Val Met Lys Val Asn Ser Phe Leu Ala					
	225		230		235
Thr Asp Pro Arg Val Glu Val Ala Gln Leu Ser Ile Gly Asp Gly Leu					
			245		250
Thr Leu Cys Arg Arg Leu Ser					
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 ctagtgtgta tccaagagaa cacgagcaac tcaaagaact cacacaagcc tcattcgata 180
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Val Tyr Pro Arg Glu His Glu Gln Leu Lys Glu Leu Thr Gln Ala Ser
 35 40 45

Phe Asp Lys Tyr Lys Ile Val Ser Leu Met Gly Val Pro Pro Asp Glu
 50 55 60

Ala Gln Phe Leu Ser Met Leu Leu Lys Ile Met Asn Ala Lys Lys Thr
 65 70 75 80

Met Glu Ile Gly Val Phe Thr Gly Tyr Ser Leu Leu Ala Thr Ala Leu
 85 90 95

Ala Leu Pro Glu Asp Gly Lys Ile Ile Ala Ile Asp Pro Asp Arg Glu
 100 105 110

Ala Tyr Glu Val Gly Leu Pro Tyr Ile Gln Lys Ala Gly Val Glu His
 115 120 125

Lys Ile Glu Phe Ile Gln Ser Glu Ala Leu Pro Val Leu Glu Lys Leu
 130 135 140

Leu Ser Asn Gly Glu Glu Glu Gly Thr Phe Asp Phe Ile Phe Ile Asp

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145 150 155 160
 Ala Asp Lys Glu Asn Tyr Leu Lys Tyr His Glu Ile Val Leu Lys Leu
 165 170 175
 Val Lys Val Gly Gly Val Ile Gly Tyr Asp Asn Thr Leu Trp Phe Gly
 180 185 190
 Thr Val Ala Leu Ser Asp Asp Asp Pro Ile Pro Gln Gly Leu Arg Glu
 195 200 205
 Leu Arg Arg Ser Val Leu Lys Ile Asn Ser Phe Leu Ala Thr Asp Pro
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 Arg Arg Leu Ser

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<210> 10
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<213> TMT5.

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agacaagtgc ctatccacga gaacatccgc agctcaaaga actaaggagc gcaactgtgg    180
acaagtatca atattggagc ttgatgaatg ttccagctga tgaggggcag ttcatttcaa    240
tgttactgaa aattatgaac gcaaaaaaga caattgaagt tggagttttc acaggctact    300
cactcctatc aactgctctg gctctacctg atgatggcaa aatcgttgcc attgatcctg    360
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Lys Glu Leu Arg Ser Ala Thr Val Asp Lys Tyr Gln Tyr Trp Ser Leu
35           40           45

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Met Asn Val Pro Ala Asp Glu Gly Gln Phe Ile Ser Met Leu Leu Lys
 50 55 60

Ile Met Asn Ala Lys Lys Thr Ile Glu Val Gly Val Phe Thr Gly Tyr
 65 70 75 80

Ser Leu Leu Ser Thr Ala Leu Ala Leu Pro Asp Asp Gly Lys Ile Val
 85 90 95

Ala Ile Asp Pro Asp Arg Glu Ala Tyr Glu Thr Gly Leu Pro Phe Ile
 100 105 110

Lys Lys Ala Asn Val Ala His Lys Ile Gln Tyr Ile Gln Ser Asp Ala
 115 120 125

Met Lys Val Met Asn Asp Leu Ile Ala Ala Lys Gly Glu Glu Glu Glu
 130 135 140

Gly Ser Phe Asp Phe Gly Phe Val Asp Ala Asp Lys Glu Asn Tyr Ile
 145 150 155 160

Asn Tyr His Glu Lys Leu Leu Lys Leu Val Lys Val Gly Gly Ile Ile
 165 170 175

Gly Tyr Asp Asn Thr Leu Trp Ser Gly Thr Val Ala Ala Ser Glu Asp
 180 185 190

Asp Glu Asn Asn Met Arg Asp Tyr Leu Arg Gly Cys Arg Gly His Ile
 195 200 205

Leu Lys Leu Asn Ser Phe Leu Ala Asn Asp Asp Arg Ile Glu Leu Ala
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His Leu Ser Ile Gly Asp Gly Leu Thr Leu Cys Lys Arg Leu Lys
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<222> (34)..(35)

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<210> 21

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<212> DNA

<213> Fuchsia FMT

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tttattcaga aagctggagt gggacataag atcaacttca tcaatggtga cgcacttgca 180

gtactcgacg atcttattgc agacggaaaa gatcaagagg ggagttttga ttttgcgttc 240

gtggatgcta acaaggaaga ttacatcaag taccacgaac agctgcttaa acttgtaag 300

gtaggtggct tgatctgcta cgacaacacc ctgtgggttcg ggtcgggtggc gctctccgaa 360

gaagatccca tggacgagtt tatgagaagc ggcaggggtcc cgcttaggaa gttgaacgac 420

ttcctcgcaa atgacccccg tatcgagtca tgccttggtt ccacgggtga tggcctcacc 480

ctctgccgcc gccgcctcta atgcatctcg agagagttac tggcccctag ctagctagct 540

- 13 -

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 20 25 30

Glu Ala Tyr Glu Thr Gly Leu Pro Phe Ile Gln Lys Ala Gly Val Gly
 35 40 45

His Lys Ile Asn Phe Ile Asn Gly Asp Ala Leu Ala Val Leu Asp Asp
 50 55 60

Leu Ile Ala Asp Gly Lys Asp Gln Glu Gly Ser Phe Asp Phe Ala Phe
 65 70 75 80

Val Asp Ala Asn Lys Glu Asp Tyr Ile Lys Tyr His Glu Gln Leu Leu
 85 90 95

Lys Leu Val Lys Val Gly Gly Leu Ile Cys Tyr Asp Asn Thr Leu Trp
 100 105 110

Phe Gly Ser Val Ala Leu Ser Glu Glu Asp Pro Met Asp Glu Phe Met
 115 120 125

Arg Ser Gly Arg Val Pro Leu Arg Lys Leu Asn Asp Phe Leu Ala Asn
 130 135 140

Asp Pro Arg Ile Glu Ser Cys Leu Val Ser Ile Gly Asp Gly Leu Thr
 145 150 155 160

Leu Cys Arg Arg Arg Leu

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ctagtgtgta tccaagagaa cagcagcaac tcaaagaact cacacaagcc tcattcgata 180

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gatcggtttt gaagatcaac agtttttttag ctactgatcc tcgcattgaa ttagctcatc      720
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atagtatgca tttgcatttt ggtaattttc gcatgtagtg ttgaaatgtg aattaccaaa    1020
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<212> DNA
<213> Ad1

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<210> 28
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24

<210> 33
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<400> 33
agtctcataa gcttctctat

20

<210> 34
<211> 22
<212> DNA
<213> FucR1

<400> 34
gcaagtgcag tgcaaagaag ag

22

<210> 35
<211> 20
<212> DNA
<213> FucR3

<400> 35
gatcttatgt tccactccgc

20

<210> 36
<211> 20

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<212> DNA
 <213> FucR5

<400> 36
 gagagatctg accagtaagg 20

<210> 37
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 <212> DNA
 <213> FucR6

<400> 37
 ggatattttt cggccgtgac ctcc 24

<210> 38
 <211> 24
 <212> DNA
 <213> FucF1

<400> 38
 atcttagaga cgactgctta tccc 24

<210> 39
 <211> 68
 <212> DNA
 <213> Tor-5' pos

<400> 39
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 caaagtat 68

<210> 40
 <211> 63
 <212> DNA
 <213> Tor-5' neg

<400> 40
 tactttgcga gggcttcgct ctgcaaaatg gtgccataga acttatcttt catttttgct 60
 gcg 63

<210> 41
 <211> 841
 <212> DNA
 <213> Fuchsia FMT (3282)

<400> 41
 atcttagaga cgactgctta tcccggagaa aatgagcatc tgaagcaact ccgggaggtc 60
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atatcgctaa tattgaagct catgaacgcg agaaagacat tagagatcgg cgtcttcact 180
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gaccccgaca aagaagctta cgagaccggg ctgccattta ttcagaaagc tggagtggaa 300
cataagatca acttcatcaa tggtgacgca cttgcagtac tcgacgatct tattgcagac 360
ggaaaagatc aagaggggag ttttgatttt gcgttcgtgg atgctaacaa ggaagattac 420
atcaagtacc acgaacagct gcttaaactg gtcaaggtag gtggcttgat ctgctacgac 480
aacaccctgt gggtcgggtc ggtggcgctc tccgaagaag atcccatgga tgagtttatg 540
aggagcggca ggggtcccaat taggaagttg aacgacttcc tcgcaaata ccccggtatc 600
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atctcgagag agttactggc ccctagctag ctagctcggt gttgttatat atatataatta 720
tccgattgat atgtggattc tcaccatatg taogtggatt ctgtgtacta tccagtggcg 780
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<210> 42
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<213> Fuchsia FMT (3282)

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<400> 42

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Ile Leu Glu Thr Thr Ala Tyr Pro Gly Glu Asn Glu His Leu Lys Gln
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Leu Arg Glu Val Thr Ala Glu Lys Tyr Pro Tyr Trp Ser Met Met Asn
          20           25           30

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```

Val Ser Ile Asp Glu Gly Gln Leu Ile Ser Leu Ile Leu Lys Leu Met
35           40           45

```

```

Asn Ala Arg Lys Thr Leu Glu Ile Gly Val Phe Thr Gly Tyr Ser Leu
50           55           60

```

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Leu Cys Thr Ala Leu Ala Leu Pro Pro Asp Gly Lys Ile Thr Ala Ile
65           70           75           80

```

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Asp Pro Asp Lys Glu Ala Tyr Glu Thr Gly Leu Pro Phe Ile Gln Lys
85           90           95

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Ala Gly Val Glu His Lys Ile Asn Phe Ile Asn Gly Asp Ala Leu Ala
 100 105 110

Val Leu Asp Asp Leu Ile Ala Asp Gly Lys Asp Gln Glu Gly Ser Phe
 115 120 125

Asp Phe Ala Phe Val Asp Ala Asn Lys Glu Asp Tyr Ile Lys Tyr His
 130 135 140

Glu Gln Leu Leu Lys Leu Val Lys Val Gly Gly Leu Ile Cys Tyr Asp
 145 150 155 160

Asn Thr Leu Trp Phe Gly Ser Val Ala Leu Ser Glu Glu Asp Pro Met
 165 170 175

Asp Glu Phe Met Arg Ser Gly Arg Val Pro Ile Arg Lys Leu Asn Asp
 180 185 190

Phe Leu Ala Asn Asp Pro Arg Ile Glu Ser Cys Leu Val Ser Ile Gly
 195 200 205

Asp Gly Ile Thr Leu Cys Arg Arg Arg Leu
 210 215

<210> 43

<211> 943

<212> DNA

<213> Fuchsia FMT full (3289)

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 gggaggtcac ggccgaaaaa tctccttact ggagcatgat gaatgtgtca attgacgagg 180
 gacaacttat atcgctaata ttgaagctca tgaacgcgag aaagacatta gagatcggcg 240
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 cagcgatcga ccccgacaaa gaagcttacg agaccgggct gccatttatt cagaaagctg 360
 gagtggaaca taagatcaac ttcacatcaatg gtgacgcact tgcagtactc gacgatctta 420
 ttgcagacgg aaaagatcaa gaggggagtt ttgattttgc gttcgtggat gctaacaagg 480
 aagattacat caagtaccac gaacagctgc ttaaactggt caaggtaggt ggcttgatct 540

- 21 -

gctacgacaa caccctgtgg ttccgggtcgg tggcgctctc cgaagaagat cccatggatg 600
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 cccgtatcga gtcatgcctt gtttccatcg gtgatggcat caccctctgc cgccgcgcgc 720
 tctaatagcat ctcgagagag ttactggccc ctagctagct agctcgttgt tgttatatat 780
 atatattatc cgattgatat gtggattctc accatatgta cgtggattct gtgtactatc 840
 cagtggcgcc ttttggtgca tctatctata tttctagttt attttatgta ccaaaaaaaaa 900
 aaaaaaaaaag cttgttctac agctcgagac tagttctctc aaa 943

<210> 44
 <211> 236
 <212> PRT
 <213> Fuchsia FMT full (3289)

<400> 44

Met Lys Asp Lys Phe Tyr Gly Thr Ile Leu Gln Ser Glu Ala Leu Ala
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Lys Tyr Ile Leu Glu Thr Thr Ala Tyr Pro Gly Glu Asn Glu His Leu
 20 25 30

Lys Gln Leu Arg Glu Val Thr Ala Glu Lys Tyr Pro Tyr Trp Ser Met
 35 40 45

Met Asn Val Ser Ile Asp Glu Gly Gln Leu Ile Ser Leu Ile Leu Lys
 50 55 60

Leu Met Asn Ala Arg Lys Thr Leu Glu Ile Gly Val Phe Thr Gly Tyr
 65 70 75 80

Ser Leu Leu Cys Thr Ala Leu Ala Leu Pro Pro Asp Gly Lys Ile Thr
 85 90 95

Ala Ile Asp Pro Asp Lys Glu Ala Tyr Glu Thr Gly Leu Pro Phe Ile
 100 105 110

Gln Lys Ala Gly Val Glu His Lys Ile Asn Phe Ile Asn Gly Asp Ala
 115 120 125

Leu Ala Val Leu Asp Asp Leu Ile Ala Asp Gly Lys Asp Gln Glu Gly
 130 135 140

- 22 -

Ser Phe Asp Phe Ala Phe Val Asp Ala Asn Lys Glu Asp Tyr Ile Lys
 145 150 155 160

Tyr His Glu Gln Leu Leu Lys Leu Val Lys Val Gly Gly Leu Ile Cys
 165 170 175

Tyr Asp Asn Thr Leu Trp Phe Gly Ser Val Ala Leu Ser Glu Glu Asp
 180 185 190

Pro Met Asp Glu Phe Met Arg Ser Gly Arg Val Pro Ile Arg Lys Leu
 195 200 205

Asn Asp Phe Leu Ala Asn Asp Pro Arg Ile Glu Ser Cys Leu Val Ser
 210 215 220

Ile Gly Asp Gly Ile Thr Leu Cys Arg Arg Arg Leu
 225 230 235

<210> 45
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<400> 45
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8

<210> 46
 <211> 8
 <212> DNA
 <213> oligonucleotide

<400> 46
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8

<210> 47
 <211> 8
 <212> DNA
 <213> oligonucleotide

<400> 47
 ggatcgacc

8